

SEQUENCE LISTING

AP20 Rec'd PCT/PTO 16 DEC 2005

<110> Advanced Technologies (Cambridge) Ltd

<120> Plant Limit Dextrinase Inhibitor

<130> RD-ATC-32

<140>

<141>

<160> 25

<170> PatentIn Ver. 2.1

<210> 1

<211> 517

<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (14)..(457)

<400> 1

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actagtatca aca atg gca tcc gac cat cgt cgc ttc gtc ctc tcc ggc      49
      Met Ala Ser Asp His Arg Arg Phe Val Leu Ser Gly
            1             5             10

gcc gtc ttg ctc tcg gtc ctc gcc gtc gcc gcc gcc acc ctg gag agc      97
Ala Val Leu Leu Ser Val Leu Ala Val Ala Ala Ala Thr Leu Glu Ser
            15             20             25

gtc aag gac gag tgc caa cca ggg gtg gac ttc ccg cat aac ccg tta      145
Val Lys Asp Glu Cys Gln Pro Gly Val Asp Phe Pro His Asn Pro Leu
            30             35             40

gcc acc tgc cac acc tac gtg ata aaa cgg gtc tgc ggc cgc ggt ccc      193,
Ala Thr Cys His Thr Tyr Val Ile Lys Arg Val Cys Gly Arg Gly Pro
            45             50             55             60

agc cgg ccc atg ctg gtg aag gag cgg tgc tgc cgg gag ctg gcg gcc      241
Ser Arg Pro Met Leu Val Lys Glu Arg Cys Cys Arg Glu Leu Ala Ala
            65             70             75

gtc ccg gat cac tgc cgg tgc gag gcg ctg cgc atc ctc atg gac ggg      289
Val Pro Asp His Cys Arg Cys Glu Ala Leu Arg Ile Leu Met Asp Gly
            80             85             90

gtg cgc acg ccg gag ggc cgc gtg gtt gag gga cgg ctc ggt gac agg      337
Val Arg Thr Pro Glu Gly Arg Val Val Glu Gly Arg Leu Gly Asp Arg
            95             100             105

cgt gac tgc ccg agg gag gag cag agg gcg ttc gcc gcc acg ctt gtc      385
Arg Asp Cys Pro Arg Glu Glu Gln Arg Ala Phe Ala Ala Thr Leu Val
            110             115             120

acg gcg gcg gag tgc aac cta tcg tcc gtc cag gag ccg gga gta cgc      433
Thr Ala Ala Glu Cys Asn Leu Ser Ser Val Gln Glu Pro Gly Val Arg
            125             130             135             140

```

ttg gtg cta ctg gca gat gga tga cgatcgaaat ggcgccaaggt aatgaagcgg 487.
 Leu Val Leu Leu Ala Asp Gly
 145

agtactgtat acagaataaaa agtactcgag 517

<210> 2
 <211> 147
 <212> PRT
 <213> Hordeum vulgare

<400> 2
 Met Ala Ser Asp His Arg Arg Phe Val Leu Ser Gly Ala Val Leu Leu
 1 5 10 15
 Ser Val Leu Ala Val Ala Ala Ala Thr Leu Glu Ser Val Lys Asp Glu
 20 25 30
 Cys Gln Pro Gly Val Asp Phe Pro His Asn Pro Leu Ala Thr Cys His
 35 40 45
 Thr Tyr Val Ile Lys Arg Val Cys Gly Arg Gly Pro Ser Arg Pro Met
 50 55 60
 Leu Val Lys Glu Arg Cys Cys Arg Glu Leu Ala Val Pro Asp His
 65 70 75 80
 Cys Arg Cys Glu Ala Leu Arg Ile Leu Met Asp Gly Val Arg Thr Pro
 85 90 95
 Glu Gly Arg Val Val Glu Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro
 100 105 110
 Arg Glu Glu Gln Arg Ala Phe Ala Ala Thr Leu Val Thr Ala Ala Glu
 115 120 125
 Cys Asn Leu Ser Ser Val Gln Glu Pro Gly Val Arg Leu Val Leu Leu
 130 135 140
 Ala Asp Gly
 145

<210> 3
 <211> 672
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (39)..(482)

<400> 3
 aagagattga accaacgacc aataaactag tatcaaca atg gca tcc gac cat cgt 56
 Met Ala Ser Asp His Arg
 1 5
 cgc ttc gtc ctc tcc ggc gcc gtc ttg ctc tcg gtc ctc gcc gtc gcc 104
 Arg Phe Val Leu Ser Gly Ala Val Leu Leu Ser Val Leu Ala Val Ala
 10 15 20
 gcc gcc acc ttg gag agc gtc aag gac gag tgc caa cta ggg gtg gac 152
 Ala Ala Thr Leu Glu Ser Val Lys Asp Glu Cys Gln Leu Gly Val Asp
 25 30 35
 ttc ccg cat aac ccg tta gcc acc tgc cac acc tac gtg ata aaa cgg 200
 Phe Pro His Asn Pro Leu Ala Thr Cys His Thr Tyr Val Ile Lys Arg
 40 45 50

```

gtc tgc ggc cgc ggt ccc agc cgg ccc atg ctg gtg aag gag cgg tgc 248
Val Cys Gly Arg Gly Pro Ser Arg Pro Met Leu Val Lys Glu Arg Cys
55 60 65 70

tgc cgg gag ctg gcg gcc gtc ccg gat cac tgc cgg tgc gag gcg ctg 296
Cys Arg Glu Leu Ala Val Pro Asp His Cys Arg Cys Glu Ala Leu
75 80 85

cgc atc ctc atg gac ggg gtg cgc acg ccg gag ggc cgc gtg gtt gag 344
Arg Ile Leu Met Asp Gly Val Arg Thr Pro Glu Gly Arg Val Val Glu
90 95 100

gga cgg ctc ggt gac agg cgt gac tgc ccg agg gag gag cag agg gcg 392
Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro Arg Glu Glu Gln Arg Ala
105 110 115

ttc gcc gcc acg ctt gtc acg gcg gcg gag tgc aac cta tcg tcc gtc 440
Phe Ala Ala Thr Leu Val Thr Ala Ala Glu Cys Asn Leu Ser Ser Val
120 125 130

cag gcg ccg gga gta cgc ttg gtg cta ctg gca gat gga tga 482
Gln Ala Pro Gly Val Arg Leu Val Leu Leu Ala Asp Gly
135 140 145

cgatgcaaat gcgccaaggt aatgaagcgg agtactgtat acagaataaa agtactcgag 542

tgaaaacaaa ctcataaata aaccttgtga gatgtatgcg tatgatctat ggtgtggaca 602

gttaaattgt ggccgattga tgaataaaaa aggttgggaac aaattaaatt gttgtggggt 662

catatactat 672

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<210> 4

<211> 147

<212> PRT

<213> Hordeum vulgare

<400> 4

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Met Ala Ser Asp His Arg Arg Phe Val Leu Ser Gly Ala Val Leu Leu
1 5 10 15
Ser Val Leu Ala Val Ala Ala Ala Thr Leu Glu Ser Val Lys Asp Glu
20 25 30
Cys Gln Leu Gly Val Asp Phe Pro His Asn Pro Leu Ala Thr Cys His
35 40 45
Thr Tyr Val Ile Lys Arg Val Cys Gly Arg Gly Pro Ser Arg Pro Met
50 55 60
Leu Val Lys Glu Arg Cys Cys Arg Glu Leu Ala Ala Val Pro Asp His
65 70 75 80
Cys Arg Cys Glu Ala Leu Arg Ile Leu Met Asp Gly Val Arg Thr Pro
85 90 95
Glu Gly Arg Val Val Glu Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro
100 105 110
Arg Glu Glu Gln Arg Ala Phe Ala Ala Thr Leu Val Thr Ala Ala Glu
115 120 125
Cys Asn Leu Ser Ser Val Gln Ala Pro Gly Val Arg Leu Val Leu Leu
130 135 140
Ala Asp Gly
145

```


<210> 6
 <211> 153
 <212> PRT
 <213> Triticum aestivum

<400> 6
 Met Ala Ser Asn His Arg Arg Phe Leu Leu Ser Gly Ala Val Leu Leu
 1 5 10 15
 Ser Val Leu Ala Ala Val Ala Ala Leu Glu Ser Val Glu Asp Glu Cys
 20 25 30
 Gln Pro Gly Val Ala Phe Pro His Asn Ala Leu Ala Thr Cys His Thr
 35 40 45
 Tyr Val Ile Lys Arg Val Cys Gly Arg Gly Pro Ser Arg Pro Met Leu
 50 55 60
 Val Lys Glu Arg Cys Cys Arg Glu Leu Ala Val Val Pro Asp Tyr Cys
 65 70 75 80
 Arg Cys Glu Ala Leu Arg Val Leu Met Asp Gly Val Arg Ala Glu Glu
 85 90 95
 Gly His Val Val Glu Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro Arg
 100 105 110
 Glu Ala Gln Arg Glu Phe Ala Ala Thr Leu Val Thr Ala Ala Glu Cys
 115 120 125
 Asn Leu Pro Thr Val Ser Gly Val Gly Ser Thr Leu Gly Ala Thr Gly
 130 135 140
 Arg Trp Met Thr Ile Glu Leu Pro Lys
 145 150

<210> 7
 <211> 444
 <212> DNA

<213> Hordeum spontaneum

<220>
 <221> CDS
 <222> (1)..(444)

<400> 7
 atg gcg ttc aag tac cag ctc ctc ctc tcg gcc gcc gtc atg ctc gcc 48
 Met Ala Phe Lys Tyr Gln Leu Leu Leu Ser Ala Ala Val Met Leu Ala
 1 5 10 15
 att ctc gcc gcc act gtc acc agt ttc ggg gat atg tgt gct cca ggg 96
 Ile Leu Ala Ala Thr Val Thr Ser Phe Gly Asp Met Cys Ala Pro Gly
 20 25 30
 gat gcg ttg cca gcc aac cct ctc aga gcc tgc cgc acc tat gtg gtt 144
 Asp Ala Leu Pro Ala Asn Pro Leu Arg Ala Cys Arg Thr Tyr Val Val
 35 40 45
 agt caa atc tgc cat gta ggc cct aga cta tcc acc tgg gac atg aag 192
 Ser Gln Ile Cys His Val Gly Pro Arg Leu Ser Thr Trp Asp Met Lys
 50 55 60
 agg cgg tgc tgc gac gag ctg tcg gcc atc ccg gcg tac tgc aga tgc 240
 Arg Arg Cys Cys Asp Glu Leu Ser Ala Ile Pro Ala Tyr Cys Arg Cys
 65 70 75 80

```

gag gcg ctg cgt atc atc atg gat ggg aca gta act tgg cag ggt gtg 288
Glu Ala Leu Arg Ile Ile Met Asp Gly Thr Val Thr Trp Gln Gly Val
      85                      90                      95

ttc ggt gcc tac ttc aag gac atg ccc aac tgc cct agg gtg atg caa 336
Phe Gly Ala Tyr Phe Lys Asp Met Pro Asn Cys Pro Arg Val Met Gln
      100                      105                      110

acg agc tac gcc gcc aac ctc gtc aac cgg cag gag tgc aac cta tgg 384
Thr Ser Tyr Ala Ala Asn Leu Val Asn Pro Gln Glu Cys Asn Leu Trp
      115                      120                      125

act atc cac ggc agc cgg tcc tgc ccc gaa ctg cag ccc gga tat gaa 432
Thr Ile His Gly Ser Pro Ser Cys Pro Glu Leu Gln Pro Gly Tyr Glu
      130                      135                      140

gtg gtc ttg taa 444
Val Val Leu
145

```

```

<210> 8
<211> 147
<212> PRT
<213> Hordeum spontaneum

```

```

<400> 8
Met Ala Phe Lys Tyr Gln Leu Leu Leu Ser Ala Ala Val Met Leu Ala
  1           5           10           15
Ile Leu Ala Ala Thr Val Thr Ser Phe Gly Asp Met Cys Ala Pro Gly
      20           25           30
Asp Ala Leu Pro Ala Asn Pro Leu Arg Ala Cys Arg Thr Tyr Val Val
      35           40           45
Ser Gln Ile Cys His Val Gly Pro Arg Leu Ser Thr Trp Asp Met Lys
      50           55           60
Arg Arg Cys Cys Asp Glu Leu Ser Ala Ile Pro Ala Tyr Cys Arg Cys
      65           70           75           80
Glu Ala Leu Arg Ile Ile Met Asp Gly Thr Val Thr Trp Gln Gly Val
      85           90           95
Phe Gly Ala Tyr Phe Lys Asp Met Pro Asn Cys Pro Arg Val Met Gln
      100          105          110
Thr Ser Tyr Ala Ala Asn Leu Val Asn Pro Gln Glu Cys Asn Leu Trp
      115          120          125
Thr Ile His Gly Ser Pro Ser Cys Pro Glu Leu Gln Pro Gly Tyr Glu
      130          135          140
Val Val Leu
145

```

```

<210> 9
<211> 483
<212> DNA
<213> Oryza sativa

```

```

<220>
<221> CDS
<222> (1)..(483)

```

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<400> 9

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atg gct tcc aac aag gta gtg ttc tca gtg ttg ctt ctc gcc gtc gtc 48
Met Ala Ser Asn Lys Val Val Phe Ser Val Leu Leu Leu Ala Val Val
1 5 10 15

tcc gtg ctc gcg gcg acg gcg acc atg gcg gag tac cac cac caa gac 96
Ser Val Leu Ala Ala Thr Ala Thr Met Ala Glu Tyr His His Gln Asp
20 25 30

cag gtg gtc tac acc ccg gcc ccg ctc tgt cag cca gga atg gcc tac 144
Gln Val Val Tyr Thr Pro Gly Pro Leu Cys Gln Pro Gly Met Gly Tyr
35 40 45

ccg atg tac ccg ctc ccg cgt tgc ccg gcg ttg gtg aag cgc cag tgc 192
Pro Met Tyr Pro Leu Pro Arg Cys Arg Ala Leu Val Lys Arg Gln Cys
50 55 60

gtc gcc cgt gcc acg gcc gcc gcc gcc gag cag gtc ccg cga gac tgc 240
Val Gly Arg Gly Thr Ala Ala Ala Ala Glu Gln Val Arg Arg Asp Cys
65 70 75 80

tgc cgg cag ctc gcc gcc gtc gac gac agc tgg tgc agg tgc gag gcg 288
Cys Arg Gln Leu Ala Ala Val Asp Asp Ser Trp Cys Arg Cys Glu Ala
85 90 95

atc agc cac atg ctg gga gcc atc tac agg gag ctc gcc gcc ccc gat 336
Ile Ser His Met Leu Gly Gly Ile Tyr Arg Glu Leu Gly Ala Pro Asp
100 105 110

gtc ggg cac ccc atg tcc gag gtg ttc cgc gcc tgc ccg aga ggg gac 384
Val Gly His Pro Met Ser Glu Val Phe Arg Gly Cys Arg Arg Gly Asp
115 120 125

ttg gag cgc gcg gcg gcg agc ctc ccg gcg ttc tgc aac gtg gac atc 432
Leu Glu Arg Ala Ala Ala Ser Leu Pro Ala Phe Cys Asn Val Asp Ile
130 135 140

ccc aac gcc gga ggt ggt gtc tgc tac tgg ctg gcg aga tct gcc tac 480
Pro Asn Gly Gly Gly Val Cys Tyr Trp Leu Ala Arg Ser Gly Tyr
145 150 155 160

tag 483

```

<210> 10
 <211> 160
 <212> PRT
 <213> *Oryza sativa*

<400> 10
 Met Ala Ser Asn Lys Val Val Phe Ser Val Leu Leu Leu Ala Val Val
 1 5 10 15
 Ser Val Leu Ala Ala Thr Ala Thr Met Ala Glu Tyr His His Gln Asp
 20 25 30
 Gln Val Val Tyr Thr Pro Gly Pro Leu Cys Gln Pro Gly Met Gly Tyr
 35 40 45
 Pro Met Tyr Pro Leu Pro Arg Cys Arg Ala Leu Val Lys Arg Gln Cys
 50 55 60
 Val Gly Arg Gly Thr Ala Ala Ala Ala Glu Gln Val Arg Arg Asp Cys
 65 70 75 80
 Cys Arg Gln Leu Ala Ala Val Asp Asp Ser Trp Cys Arg Cys Glu Ala

				85				90					95				
Ile	Ser	His	Met	Leu	Gly	Gly	Ile	Tyr	Arg	Glu	Leu	Gly	Ala	Pro	Asp		
			100					105					110				
Val	Gly	His	Pro	Met	Ser	Glu	Val	Phe	Arg	Gly	Cys	Arg	Arg	Gly	Asp		
		115					120					125					
Leu	Glu	Arg	Ala	Ala	Ala	Ser	Leu	Pro	Ala	Phe	Cys	Asn	Val	Asp	Ile		
	130					135					140						
Pro	Asn	Gly	Gly	Gly	Gly	Val	Cys	Tyr	Trp	Leu	Ala	Arg	Ser	Gly	Tyr		
145					150					155					160		

<210> 11

<211> 707

<212> DNA

<213> Triticum durum

<220>

<221> CDS

<222> (27)..(533)

<400> 11

agcgaaccag acttggctag aatacc atg gcg tgc aag tcc agc tgc agc ctc 53
 Met Ala Cys Lys Ser Ser Cys Ser Leu
 1 5

ctc ctc ttg gcc gcc gtc ctg ctc tcc gtc ttg gcc gct gct tcc gcc 101
 Leu Leu Leu Ala Ala Val Leu Leu Ser Val Leu Ala Ala Ala Ser Ala
 10 15 20 25

tcc ggc agc tgc gtc cca ggg gtg gct ttt cgg acc aat ctt ctg cca 149
 Ser Gly Ser Cys Val Pro Gly Val Ala Phe Arg Thr Asn Leu Leu Pro
 30 35 40

cac tgc cgc gac tat gtg tta caa caa act tgt ggc acc ttc acc cct 197
 His Cys Arg Asp Tyr Val Leu Gln Gln Thr Cys Gly Thr Phe Thr Pro
 45 50 55

ggg tca aag tta ccc gaa tgg atg aca tct gcg tgc ata tac tcc cct 245
 Gly Ser Lys Leu Pro Glu Trp Met Thr Ser Ala Ser Ile Tyr Ser Pro
 60 65 70

ggg aaa ccg tac ctc gcc aag ttg tat tgc tgc cag gag ctc gca gaa 293
 Gly Lys Pro Tyr Leu Ala Lys Leu Tyr Cys Cys Gln Glu Leu Ala Glu
 75 80 85

att tct cag cag tgc cgg tgc gag gcg ctg cgc tac ttc ata gcg ttg 341
 Ile Ser Gln Gln Cys Arg Cys Glu Ala Leu Arg Tyr Phe Ile Ala Leu
 90 95 100 105

ccg gta ccg tct cag cct gtg gac ccg agg tcc ggc aat gtt ggt gag 389
 Pro Val Pro Ser Gln Pro Val Asp Pro Arg Ser Gly Asn Val Gly Glu
 110 115 120

agc ggc ctc atc gat ctg ccc gga tgc ccc agg gag atg caa tgg gac 437
 Ser Gly Leu Ile Asp Leu Pro Gly Cys Pro Arg Glu Met Gln Trp Asp
 125 130 135

ttc gtc aga tta ctc gtc gcc ccg ggg cag tgc aac ttg gcg acc att 485
 Phe Val Arg Leu Leu Val Ala Pro Gly Gln Cys Asn Leu Ala Thr Ile
 140 145 150

cac aat gtt cga tac tgc ccc gcc gtg gaa cag cct ctg tgg atc tag 533
 His Asn Val Arg Tyr Cys Pro Ala Val Glu Gln Pro Leu Trp Ile
 155 160 165

agataaaatc agtcgctcgt gaataagcat gcatgttgca tccataggcg tgtggtgtgc 593
 atgtatacat atgtgagctc cgcgcgctca acatgtgtgg gctatctgct atgaatgaga 653
 ataaagagaa tcattctgtg gttctttaat ttcaactaaa aaaaaaaaaa aaaa 707

<210> 12
 <211> 168
 <212> PRT
 <213> Triticum durum

<400> 12
 Met Ala Cys Lys Ser Ser Cys Ser Leu Leu Leu Leu Ala Ala Val Leu
 1 5 10 15
 Leu Ser Val Leu Ala Ala Ala Ser Ala Ser Gly Ser Cys Val Pro Gly
 20 25 30
 Val Ala Phe Arg Thr Asn Leu Leu Pro His Cys Arg Asp Tyr Val Leu
 35 40 45
 Gln Gln Thr Cys Gly Thr Phe Thr Pro Gly Ser Lys Leu Pro Glu Trp
 50 55 60
 Met Thr Ser Ala Ser Ile Tyr Ser Pro Gly Lys Pro Tyr Leu Ala Lys
 65 70 75 80
 Leu Tyr Cys Cys Gln Glu Leu Ala Glu Ile Ser Gln Gln Cys Arg Cys
 85 90 95
 Glu Ala Leu Arg Tyr Phe Ile Ala Leu Pro Val Pro Ser Gln Pro Val
 100 105 110
 Asp Pro Arg Ser Gly Asn Val Gly Glu Ser Gly Leu Ile Asp Leu Pro
 115 120 125
 Gly Cys Pro Arg Glu Met Gln Trp Asp Phe Val Arg Leu Leu Val Ala
 130 135 140
 Pro Gly Gln Cys Asn Leu Ala Thr Ile His Asn Val Arg Tyr Cys Pro
 145 150 155 160
 Ala Val Glu Gln Pro Leu Trp Ile
 165

<210> 13
 <211> 712
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (33)..(500)

<400> 13
 catccatcga gaggccgtcg acaggggaat ta atg gcg tcg tcg tct agc agc 53
 Met Ala Ser Ser Ser Ser Ser
 1 5
 agc cac cgc cgc etc atc etc gca gcc gcc gtc ctg etc tcc gtg etc 101
 Ser His Arg Arg Leu Ile Leu Ala Ala Ala Val Leu Leu Ser Val Leu
 10 15 20

```

gcg gct gcc agc gcc agc gcc ggg acc tcc tgc gtg ccg ggg tgg gcc 149
Ala Ala Ala Ser Ala Ser Ala Gly Thr Ser Cys Val Pro Gly Trp Ala
    25                      30                      35

atc ccg cac aac ccg ctc ccg agc tgc cgc tgg tac gtg acc agc cgg 197
Ile Pro His Asn Pro Leu Pro Ser Cys Arg Trp Tyr Val Thr Ser Arg
    40                      45                      50                      55

acc tgc ggc atc ggg ccg cgc ctc ccg tgg ccg gag ctg aag agg aga 245
Thr Cys Gly Ile Gly Pro Arg Leu Pro Trp Pro Glu Leu Lys Arg Arg
                      60                      65                      70

tgc tgc ccg gag ctg gcg gac atc ccg gcg tac tgc ccg tgc acg gcg 293
Cys Cys Arg Glu Leu Ala Asp Ile Pro Ala Tyr Cys Arg Cys Thr Ala
                      75                      80                      85

ctg agc atc ctc atg gac ggc gcg atc ccg cct ggc ccg gac gcg cag 341
Leu Ser Ile Leu Met Asp Gly Ala Ile Pro Pro Gly Pro Asp Ala Gln
    90                      95                      100

ctg gag ggc cgc cta gag gac ctg ccg ggc tgc ccg ccg gag gtg cag 389
Leu Glu Gly Arg Leu Glu Asp Leu Pro Gly Cys Pro Arg Glu Val Gln
    105                      110                      115

agg gga ttc gcc gcc acc ctc gtc acg gag gcc gag tgc aac ctg gcc 437
Arg Gly Phe Ala Ala Thr Leu Val Thr Glu Ala Glu Cys Asn Leu Ala
    120                      125                      130                      135

acc atc agc ggc gtc gcc gaa tgc ccc tgg att ctc ggc ggc gga acg 485
Thr Ile Ser Gly Val Ala Glu Cys Pro Trp Ile Leu Gly Gly Gly Thr
                      140                      145                      150

atg ccc tcc aag taa ctgcgaagag catagtgcag gaggaatgag cttgttagcta 540
Met Pro Ser Lys
                      155

gctcatatgt ctgaataata agcacagcaa gaagatgaat gcatttctcg gatcggttcag 600

ccggaacaat aattaaaggg gatccggatt tgttcttggtg atataattaa cgattcctgt 660

tatacttgga agtagctagg ctgcgtcccca tccaatgcaa gcaaaaaaaaa aa 712

```

<210> 14

<211> 155

<212> PRT

<213> Zea mays

<400> 14

```

Met Ala Ser Ser Ser Ser Ser Ser His Arg Arg Leu Ile Leu Ala Ala
  1                      5                      10                      15
Ala Val Leu Leu Ser Val Leu Ala Ala Ala Ser Ala Ser Ala Gly Thr
                      20                      25                      30
Ser Cys Val Pro Gly Trp Ala Ile Pro His Asn Pro Leu Pro Ser Cys
                      35                      40                      45
Arg Trp Tyr Val Thr Ser Arg Thr Cys Gly Ile Gly Pro Arg Leu Pro
                      50                      55                      60
Trp Pro Glu Leu Lys Arg Arg Cys Cys Arg Glu Leu Ala Asp Ile Pro
                      65                      70                      75                      80

```

Ala	Tyr	Cys	Arg	Cys	Thr	Ala	Leu	Ser	Ile	Leu	Met	Asp	Gly	Ala	Ile
				85					90					95	
Pro	Pro	Gly	Pro	Asp	Ala	Gln	Leu	Glu	Gly	Arg	Leu	Glu	Asp	Leu	Pro
			100					105					110		
Gly	Cys	Pro	Arg	Glu	Val	Gln	Arg	Gly	Phe	Ala	Ala	Thr	Leu	Val	Thr
		115					120					125			
Glu	Ala	Glu	Cys	Asn	Leu	Ala	Thr	Ile	Ser	Gly	Val	Ala	Glu	Cys	Pro
	130					135					140				
Trp	Ile	Leu	Gly	Gly	Gly	Thr	Met	Pro	Ser	Lys					
145					150					155					

```
<210> 15
<211> 122
<212> PRT
<213> Gleusine coracana
```

```

<400> 15
Ser Val Gly Thr Ser Cys Ile Pro Gly Met Ala Ile Pro His Asn Pro
  1          5          10          15

Leu Asp Ser Cys Arg Trp Tyr Val Ala Lys Arg Ala Cys Gly Val Gly
          20          25          30

Pro Arg Leu Ala Thr Gln Glu Met Lys Ala Arg Cys Cys Arg Gln Leu
          35          40          45

Glu Ala Ile Pro Ala Tyr Cys Arg Cys Glu Ala Val Arg Ile Leu Met
  50          55          60

Asp Gly Val Val Thr Pro Ser Gly Gln His Glu Gly Arg Leu Leu Gln
  65          70          75          80

Asp Leu Pro Gly Cys Pro Arg Gln Val Gln Arg Ala Phe Ala Pro Lys
          85          90          95

Leu Val Thr Glu Val Glu Cys Asn Leu Ala Thr Ile His Gly Gly Pro
          100          105          110

Phe Cys Leu Ser Leu Leu Gly Ala Gly Glu
          115          120

```

```
<210> 16
<211> 121
<212> PRT
<213> Secale cereale
```

```

<400> 16
Ser Val Gly Gly Gln Cys Val Pro Gly Leu Ala Met Pro His Asn Pro
  1                    5                10                15

Leu Gly Ala Cys Arg Thr Tyr Val Val Ser Gln Ile Cys His Val Gly
      20          25          30

Pro Arg Leu Phe Thr Trp Asp Met Lys Arg Arg Cys Cys Asp Glu Leu
      35          40          45

Leu Ala Ile Pro Ala Tyr Cys Arg Cys Glu Ala Leu Arg Ile Leu Met
      50          55          60

```

Asp Gly Val Val Thr Gln Gln Gly Val Phe Glu Gly Gly Tyr Leu Lys
65 70 75 80
Asp Met Pro Asn Cys Pro Arg Val Thr Gln Arg Ser Tyr Ala Ala Thr
85 90 95
Leu Val Ala Pro Gln Glu Cys Asn Leu Pro Thr Ile His Gly Ser Pro
100 105 110
Tyr Cys Pro Thr Leu Gln Ala Gly Tyr
115 120

<210> 17
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 17
accaataaac tagtatcaac aatggcatcc gacca 35

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 18
ccaacctttt ttattcatca atcggccaca 30

<210> 19
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 19
tcggattcca ttgcccagct atctgtc 27

<210> 20
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 20
atgggcccta acaatcagta aattgaacg 29

<210> 21
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 21
cggtaccggc aggctgaagt cca

23

<210> 22
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 22
ccggggatct accatgagcc caga

24

<210> 23
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 23
gaatgaaccg aaaccggcgg ta

22

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 24
taccacctcc ctgagggttg

20

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 25
ccatgcctag ggtcacactt

20